Claims:

1. A method of designing a compound able to bind to a molecule of the insulin receptor family and to modulate an activity mediated by the molecule, including the step of assessing the stereochemical complementarity between the compound and the receptor site of the molecule, wherein the receptor site includes:

(a) amino acids 1 to 462 of the receptor for IGF-1, having the atomic coordinates substantially as shown in Figure 1;

(b) a subset of said amino acids, or;

(c) amino acids present in the amino acid sequence of a member of the insulin receptor family, which form an equivalent three-dimensional structure to that of the receptor molecule as depicted in Figure 1.

2. A method according to claim 1, in which the compound is selected or modified from a known compound identified from a database.

3. A method according to claim 1, in which the compound is designed so as to complement the structure of the receptor molecule as depicted in Figure 1.

4. A method according to ~~any one of~~ claim~~s~~ 1 ~~to 3~~, in which the compound has structural regions able to make close contact with amino acid residues at the surface of the receptor site lining the groove, as depicted in Figure 2.

5. A method according to ~~any one of~~ claim~~s~~ 1 ~~to 4~~, in which the compound has a stereochemistry such that it can interact with both the L1 and L2 domains of the receptor site.

6. A method according to ~~any one of~~ claim~~s~~ 1 ~~to 4~~, in which the compound has a stereochemistry such that it can interact with the L1 domain of a first monomer of the receptor homodimer, and with the L2 domain of the other monomer of the receptor homodimer.

7. A method according to ~~any one of~~ claim~~s~~ 1 ~~to 4~~, in which the interaction of the compound with the receptor site alters the position of at least one of the

L1, L2 or cysteine-rich domains of the receptor molecule relative to the position of at least one of the other of said domains.

8. A method according to claim 7, in which the compound interacts with the β sheet of the L1 domain of the receptor molecule, thereby causing an alteration in the position of the L1 domain relative to the position of the cysteine-rich domain or of the L2 domain.

9. A method according to claim 7, in which the compound interacts with the receptor site in the region of the interface between the L1 domain an the cysteine-rich domain of the receptor molecule, thereby causing the L1 domain and the cysteine-rich domain to move away from each other.

10. A method according to claim 7, in which the compound interacts with the hinge region between the L2 domain and the cysteine-rich domain of the receptor molecule, thereby causing an alteration in the positions of the L2 domain and the cysteine-rich domain relative to each other.

11. A method according to ~~any one of~~ claim~~s~~ 1 ~~to 10~~, in which the stereochemical complementarity between the compound and the receptor site is such that the compound has a K_i for the receptor side of less than 10^{-6}M.

12. A method according to claim 11, in which the K_i is less than 10^{-8}M.

13. A method according to ~~any one of~~ claim~~s~~ 1 ~~to 12~~, in which the compound has the ability to increase an activity mediated by the receptor molecule.

14. A method according to ~~any one of~~ claim~~s~~ 1 ~~to 12~~, in which the compound has the ability to decrease an activity mediated by the receptor molecule.

15. A method according to claim 14, in which the stereochemical interaction between the compound and the receptor site is adapted to prevent the binding of a natural ligand of the receptor molecule to the receptor site.

16. A method according to claim 14 ~~or claim 15~~, in which the compound has a K_1 of less than 10^{-6}M.

17. A method according to claim 16, in which the compound has a K_1 of less than 10^{-8}M.

18. A method according to claim 17, in which the compound has a K_1 of less than 10^{-9}M.

19. A method according to ~~any one of~~ claims 1 ~~to 18~~, in which the receptor is the IGF-1R.

20. A method according to ~~any one of~~ claims 1 ~~to 18~~, in which the receptor is the insulin receptor.

21. A computer-assisted method for identifying potential compounds able to bind to a molecule of the insulin receptor family and to modulate an activity mediated by the molecule, using a programmed computer including a processor, an input device, and an output device, including the steps of:

(a) inputting into the programmed computer, through the input device, data comprising the atomic coordinates of the IGF-1R molecule as shown in Figure 1, or a subset thereof;

(b) generating, using computer methods, a set of atomic coordinates of a structure that possesses stereochemical complementarity to the atomic coordinates of the IGF-1R site as shown in Figure 1, or a subset thereof, thereby generating a criteria data set;

(c) comparing, using the processor, the criteria data set to a computer database of chemical structures;

(d) selecting from the database, using computer methods, chemical structures which are structurally similar to a portion of said criteria data set; and

(e) outputting, to the output device, the selected chemical structures which are similar to a portion of the criteria data set.

22. A computer-assisted method according to claim 21, in which the method is used to identify potential compounds which have the ability to decrease an activity mediated by the receptor.

23. A computer-assisted method according to claim 21 ~~or claim 22~~, which further includes the step of selecting one or more chemical structures from step (e) which interact with the receptor site of the molecule in a manner which prevents the binding of natural ligands to the receptor site.

24. A computer-assisted method according to ~~any one of~~ claim~~s~~ 21 ~~to 23~~, which further includes the step of obtaining a compound with a chemical structure selected in steps (d) and (e), and testing the compound for the ability to decrease an activity mediated by the receptor.

25. A computer-assisted method according to claim 21, in which the method is used to identify potential compounds which have the ability to increase an activity mediated by the receptor molecule.

26. A computer-assisted method according to claim 25, further including the step of obtaining a molecule with a chemical structure selected in steps (d) and (e), and testing the compound for the ability to increase an activity mediated by the receptor.

27. A computer-assisted method according to ~~any one of~~ claim~~s~~ 21 ~~to 26~~, in which the receptor is the IGF-1R.

28. A computer-assisted method according to ~~any one of~~ claim~~s~~ 21 ~~to 26~~, in which the receptor is the insulin receptor.

29. A method of screening of a putative compound having the ability to modulate the activity of a receptor of the insulin receptor family, including the steps of identifying a putative compound by a method according to ~~any one of~~ claim~~s~~ 1 ~~to 29~~, and testing the compound for the ability to increase or decrease an activity mediated by the receptor.

30. A method according to claim 29, in which the test is carried out *in vitro*.

31. A method according to claim 29, in which the test is a high throughput assay.

32. A method according to claim 29, in which the test is carried out *in vivo*.

33. A method according to claim 30, in which the test is carried out *in vivo*.